

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/541,947  
Source: P4/10  
Date Processed by STIC: 7/21/05

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PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/541,947

DATE: 07/21/2005

TIME: 09:19:30

Input Set : D:\297-204 PCT.ST25.txt

Output Set: N:\CRF4\07212005\J541947.raw

3 <110> APPLICANT: North Carolina State University  
 4 Petite, James  
 5 Pardue, Samuel  
 7 <120> TITLE OF INVENTION: DEPLETION OF ENDOGENOUS PRIMORDIAL GERM CELLS IN AVIAN SPECIES  
 9 <130> FILE REFERENCE: 297/204 PCT  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/541,947  
 C--> 11 <141> CURRENT FILING DATE: 2005-07-08  
 11 <150> PRIOR APPLICATION NUMBER: US 60/440,424  
 12 <151> PRIOR FILING DATE: 2003-01-16  
 14 <160> NUMBER OF SEQ ID NOS: 8  
 16 <170> SOFTWARE: PatentIn version 3.2  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 1989  
 20 <212> TYPE: DNA  
 21 <213> ORGANISM: Gallus gallus  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: CDS  
 26 <222> LOCATION: (1)..(1989)  
 28 <400> SEQUENCE: 1  
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 30 Met Glu Glu Asp Trp Asp Thr Glu Leu Glu Gln Glu Ala Ala Ala Ala  
 31 1 5 10 15  
 33 tcc cag ggg cgt tct gag gag cag gcg tgg atg gct aac tct ggc aga 96  
 34 Ser Gln Gly Arg Ser Glu Glu Gln Ala Trp Met Ala Asn Ser Gly Arg  
 35 20 25 30  
 37 cca aac agc cca tcc ctc cgc ttc tcc agc aga cca agc agc ccc ttg 144  
 38 Pro Asn Ser Pro Ser Leu Arg Phe Ser Ser Arg Pro Ser Ser Pro Leu  
 39 35 40 45  
 41 tct ggc ttc cca ggc aga cca aac agc ccc ttc ttt ggc ttt agt cag 192  
 42 Ser Gly Phe Pro Gly Arg Pro Asn Ser Pro Phe Phe Gly Phe Ser Gln  
 43 50 55 60  
 45 aat aaa ggc tca ctt ggt gct aat gaa gga ctt aac aga agt ctg cct 240  
 46 Asn Lys Gly Ser Leu Gly Ala Asn Glu Gly Leu Asn Arg Ser Leu Pro  
 47 65 70 75 80  
 49 gtg cag cat gac att gga gga tat tct ggg agc aga gag tct gtt gta 288  
 50 Val Gln His Asp Ile Gly Gly Tyr Ser Gly Ser Arg Glu Ser Val Val  
 51 85 90 95  
 53 cgt caa aac aga gaa gat caa cca gtg act aga ttt ggt aga ggg agg 336  
 54 Arg Gln Asn Arg Glu Asp Gln Pro Val Thr Arg Phe Gly Arg Gly Arg  
 55 100 105 110  
 57 agt tct gga agc aga gat ttt caa gag agg aac tct gca aat gat cct 384  
 58 Ser Ser Gly Ser Arg Asp Phe Gln Glu Arg Asn Ser Ala Asn Asp Pro  
 59 115 120 125

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61	ggt atg caa gat caa ggt ttt aga aga gtt cct ggc atc ttt ggg caa	432
62	Gly Met Gln Asp Gln Gly Phe Arg Arg Val Pro Gly Ile Phe Gly Gln	
63	130 135 140	
65	agc aag tgt ttt aac agt gag gaa aga aat agt cct ctg cgt ggc agc	480
66	Ser Lys Cys Phe Asn Ser Glu Glu Arg Asn Ser Pro Leu Arg Gly Ser	
67	145 150 155 160	
69	cct ttt gcc cca gga gga aga gga gca gtt gga ggt cct gca gga gtt	528
70	Pro Phe Ala Pro Gly Gly Arg Gly Ala Val Gly Gly Pro Ala Gly Val	
71	165 170 175	
73	ctc aaa gga cgc tct gaa gaa att gat tct gga aga ggt cca aag gtg	576
74	Leu Lys Gly Arg Ser Glu Glu Ile Asp Ser Gly Arg Gly Pro Lys Val	
75	180 185 190	
77	act tat gtc ccc cct cct cca cct gaa gat gaa cag tcc atc ttt gca	624
78	Thr Tyr Val Pro Pro Pro Pro Pro Glu Asp Glu Gln Ser Ile Phe Ala	
79	195 200 205	
81	tgt tat cag tca gga att aat ttt gac aag tat gat gaa tgt gct gtt	672
82	Cys Tyr Gln Ser Gly Ile Asn Phe Asp Lys Tyr Asp Glu Cys Ala Val	
83	210 215 220	
85	gag atg tca gga ctt gac cct cca gca cca tta ctg gct ttt gaa gaa	720
86	Glu Met Ser Gly Leu Asp Pro Pro Ala Pro Leu Leu Ala Phe Glu Glu	
87	225 230 235 240	
89	gct aac ttt gct cag act tta agg aag aat ata tct aaa act gga tat	768
90	Ala Asn Phe Ala Gln Thr Leu Arg Lys Asn Ile Ser Lys Thr Gly Tyr	
91	245 250 255	
93	tca aaa ctt act cca gtg cag aag cac agc att cct gtt ata caa gca	816
94	Ser Lys Leu Thr Pro Val Gln Lys His Ser Ile Pro Val Ile Gln Ala	
95	260 265 270	
97	ggg cgg gat tta atg tca tgt gcc cag aca gga tca gga aaa aca gca	864
98	Gly Arg Asp Leu Met Ser Cys Ala Gln Thr Gly Ser Gly Lys Thr Ala	
99	275 280 285	
101	gct ttt ctt cta cca att gtg gac cgg atg atg aaa gat ggt gta act	912
102	Ala Phe Leu Leu Pro Ile Val Asp Arg Met Met Lys Asp Gly Val Thr	
103	290 295 300	
105	gca agc ttc cca aag cag caa gac cca caa tgc att att gtt gca cca	960
106	Ala Ser Phe Pro Lys Gln Gln Asp Pro Gln Cys Ile Ile Val Ala Pro	
107	305 310 315 320	
109	act aga gaa ctg ata aat cag atc ttc tta gaa gca agg aag ttt gtg	1008
110	Thr Arg Glu Leu Ile Asn Gln Ile Phe Leu Glu Ala Arg Lys Phe Val	
111	325 330 335	
113	tat ggg act tgt ata agg cct gtt gtg atc tat gga ggt aca cag aca	1056
114	Tyr Gly Thr Cys Ile Arg Pro Val Val Ile Tyr Gly Gly Thr Gln Thr	
115	340 345 350	
117	ggt cat tca atc cgt caa ata atg caa ggc tgt aat ata tta tgt gcc	1104
118	Gly His Ser Ile Arg Gln Ile Met Gln Gly Cys Asn Ile Leu Cys Ala	
119	355 360 365	
121	act cct gga agg ctt ctt gac att att gaa aaa ggg aag atc agt ttg	1152
122	Thr Pro Gly Arg Leu Leu Asp Ile Ile Glu Lys Gly Lys Ile Ser Leu	
123	370 375 380	
125	gtg gag gtg aaa tat ttg gta cta gat gaa gca gac cgc atg ctc gat	1200

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126	Val	Glu	Val	Lys	Tyr	Leu	Val	Leu	Asp	Glu	Ala	Asp	Arg	Met	Leu	Asp	
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130	Met	Gly	Phe	Gly	Leu	Asp	Met	Lys	Lys	Leu	Ile	Ser	Tyr	Pro	Glu	Met	
131					405					410						415	
133	cca	tct	aaa	gac	aga	cgt	caa	aca	tta	atg	ttt	agt	gcc	act	ttt	cct	1296
134	Pro	Ser	Lys	Asp	Arg	Arg	Gln	Thr	Leu	Met	Phe	Ser	Ala	Thr	Phe	Pro	
135				420					425					430			
137	gag	gaa	ggt	caa	agg	ctg	gct	ggt	gaa	ttt	ttg	aaa	acg	gac	tat	ata	1344
138	Glu	Glu	Val	Gln	Arg	Leu	Ala	Gly	Glu	Phe	Leu	Lys	Thr	Asp	Tyr	Ile	
139			435					440					445				
141	ttt	ctt	ggt	att	gga	aat	acc	tgt	gga	gcc	tgc	agt	gat	ggt	cag	caa	1392
142	Phe	Leu	Val	Ile	Gly	Asn	Thr	Cys	Gly	Ala	Cys	Ser	Asp	Val	Gln	Gln	
143		450					455						460				
145	aat	att	ctt	cag	ggt	ccc	cgg	tta	tcc	aag	agg	gat	aaa	cta	ata	gaa	1440
146	Asn	Ile	Leu	Gln	Val	Pro	Arg	Leu	Ser	Lys	Arg	Asp	Lys	Leu	Ile	Glu	
147	465					470					475					480	
149	att	cta	caa	agc	aca	ggt	ggt	gaa	cga	acc	atg	gtg	ttt	gtg	gac	aca	1488
150	Ile	Leu	Gln	Ser	Thr	Gly	Gly	Glu	Arg	Thr	Met	Val	Phe	Val	Asp	Thr	
151					485					490					495		
153	aag	aaa	aaa	gca	gat	tac	ctt	gca	gcc	ttt	ctt	tgt	caa	gag	aac	cta	1536
154	Lys	Lys	Lys	Ala	Asp	Tyr	Leu	Ala	Ala	Phe	Leu	Cys	Gln	Glu	Asn	Leu	
155				500					505					510			
157	cca	tcc	acc	agc	att	cat	gga	gat	agg	gaa	cag	aga	gag	aga	gag	ata	1584
158	Pro	Ser	Thr	Ser	Ile	His	Gly	Asp	Arg	Glu	Gln	Arg	Glu	Arg	Glu	Ile	
159			515					520					525				
161	gct	ctt	cgc	gat	ttc	cgt	tct	gga	aaa	tgt	caa	att	ctt	gtg	gca	act	1632
162	Ala	Leu	Arg	Asp	Phe	Arg	Ser	Gly	Lys	Cys	Gln	Ile	Leu	Val	Ala	Thr	
163		530					535						540				
165	tcg	gta	gca	tca	aga	ggc	ctg	gat	att	gaa	aat	ggt	caa	cat	ggt	att	1680
166	Ser	Val	Ala	Ser	Arg	Gly	Leu	Asp	Ile	Glu	Asn	Val	Gln	His	Val	Ile	
167	545					550				555						560	
169	aat	ttt	gat	ctc	cct	aac	acc	att	gaa	gat	tat	gta	cat	cga	att	gga	1728
170	Asn	Phe	Asp	Leu	Pro	Asn	Thr	Ile	Glu	Asp	Tyr	Val	His	Arg	Ile	Gly	
171					565					570					575		
173	cga	act	ggt	cgt	tgt	gga	aat	act	ggc	aaa	gca	ggt	tca	ttc	ttt	gat	1776
174	Arg	Thr	Gly	Arg	Cys	Gly	Asn	Thr	Gly	Lys	Ala	Val	Ser	Phe	Phe	Asp	
175				580					585					590			
177	gat	cag	tca	gat	ggc	cat	ctt	gta	caa	tca	cta	ctt	aaa	gtg	ctt	tcc	1824
178	Asp	Gln	Ser	Asp	Gly	His	Leu	Val	Gln	Ser	Leu	Leu	Lys	Val	Leu	Ser	
179			595					600					605				
181	aga	acc	cag	cag	gaa	ttc	cag	ttt	ggt	gga	aga	atg	gct	gtc	caa	aga	1872
182	Arg	Thr	Gln	Gln	Glu	Phe	Gln	Phe	Gly	Gly	Arg	Met	Ala	Val	Gln	Arg	
183		610					615						620				
185	aca	aat	att	ggt	gct	tca	act	tgg	tgc	cca	aag	gga	tta	atg	cag	gcc	1920
186	Thr	Asn	Ile	Val	Ala	Ser	Thr	Trp	Cys	Pro	Lys	Gly	Leu	Met	Gln	Ala	
187	625					630					635					640	
189	gtg	gca	gaa	tgg	aac	cca	aga	gaa	atg	agg	atg	tca	tat	tct	gaa	aca	1968
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213 Pro Asn Ser Pro Ser Leu Arg Phe Ser Ser Arg Pro Ser Ser Pro Leu
214          35          40          45
217 Ser Gly Phe Pro Gly Arg Pro Asn Ser Pro Phe Phe Gly Phe Ser Gln
218 50          55          60
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222 65          70          75          80
225 Val Gln His Asp Ile Gly Gly Tyr Ser Gly Ser Arg Glu Ser Val Val
226          85          90          95
229 Arg Gln Asn Arg Glu Asp Gln Pro Val Thr Arg Phe Gly Arg Gly Arg
230          100         105         110
233 Ser Ser Gly Ser Arg Asp Phe Gln Glu Arg Asn Ser Ala Asn Asp Pro
234          115         120         125
237 Gly Met Gln Asp Gln Gly Phe Arg Arg Val Pro Gly Ile Phe Gly Gln
238 130         135         140
241 Ser Lys Cys Phe Asn Ser Glu Glu Arg Asn Ser Pro Leu Arg Gly Ser
242 145         150         155         160
245 Pro Phe Ala Pro Gly Gly Arg Gly Ala Val Gly Gly Pro Ala Gly Val
246          165         170         175
249 Leu Lys Gly Arg Ser Glu Glu Ile Asp Ser Gly Arg Gly Pro Lys Val
250          180         185         190
253 Thr Tyr Val Pro Pro Pro Pro Pro Glu Asp Glu Gln Ser Ile Phe Ala
254          195         200         205
257 Cys Tyr Gln Ser Gly Ile Asn Phe Asp Lys Tyr Asp Glu Cys Ala Val
258 210         215         220
261 Glu Met Ser Gly Leu Asp Pro Pro Ala Pro Leu Leu Ala Phe Glu Glu
262 225         230         235         240
265 Ala Asn Phe Ala Gln Thr Leu Arg Lys Asn Ile Ser Lys Thr Gly Tyr
266          245         250         255
269 Ser Lys Leu Thr Pro Val Gln Lys His Ser Ile Pro Val Ile Gln Ala
270          260         265         270
273 Gly Arg Asp Leu Met Ser Cys Ala Gln Thr Gly Ser Gly Lys Thr Ala
274          275         280         285
277 Ala Phe Leu Leu Pro Ile Val Asp Arg Met Met Lys Asp Gly Val Thr
278 290         295         300
281 Ala Ser Phe Pro Lys Gln Gln Asp Pro Gln Cys Ile Ile Val Ala Pro
282 305         310         315         320

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294          355          360          365
297 Thr Pro Gly Arg Leu Leu Asp Ile Ile Glu Lys Gly Lys Ile Ser Leu
298          370          375          380
301 Val Glu Val Lys Tyr Leu Val Leu Asp Glu Ala Asp Arg Met Leu Asp
302 385          390          395          400
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306          405          410          415
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314          435          440          445
317 Phe Leu Val Ile Gly Asn Thr Cys Gly Ala Cys Ser Asp Val Gln Gln
318          450          455          460
321 Asn Ile Leu Gln Val Pro Arg Leu Ser Lys Arg Asp Lys Leu Ile Glu
322 465          470          475          480
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326          485          490          495
329 Lys Lys Lys Ala Asp Tyr Leu Ala Ala Phe Leu Cys Gln Glu Asn Leu
330          500          505          510
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334          515          520          525
337 Ala Leu Arg Asp Phe Arg Ser Gly Lys Cys Gln Ile Leu Val Ala Thr
338          530          535          540
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342 545          550          555          560
345 Asn Phe Asp Leu Pro Asn Thr Ile Glu Asp Tyr Val His Arg Ile Gly
346          565          570          575
349 Arg Thr Gly Arg Cys Gly Asn Thr Gly Lys Ala Val Ser Phe Phe Asp
350          580          585          590
353 Asp Gln Ser Asp Gly His Leu Val Gln Ser Leu Leu Lys Val Leu Ser
354          595          600          605
357 Arg Thr Gln Gln Glu Phe Gln Phe Gly Gly Arg Met Ala Val Gln Arg
358          610          615          620
361 Thr Asn Ile Val Ala Ser Thr Trp Cys Pro Lys Gly Leu Met Gln Ala
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369 Thr Phe Lys Ser Trp Glu
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373 <210> SEQ ID NO: 3
374 <211> LENGTH: 16
375 <212> TYPE: PRT
376 <213> ORGANISM: Gallus gallus
378 <400> SEQUENCE: 3

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date